

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: BASF Aktiengesellschaft
- (B) STREET: Carl-Bosch-Strasse 38
- (C) CITY: Ludwigshafen
- (E) COUNTRY: Federal Republic of Germany
- (F) POSTAL CODE: D-67056
- (G) TELEPHONE: 0621/6048526
- (H) TELEFAX: 0621/6043123
- (I) TELEX: 1762175170

(ii) TITLE OF APPLICATION: Genes of purine biosynthesis from *Ashbya gossypii* and their use in microbial riboflavin biosynthesis

(iii) NUMBER OF SEQUENCES: 13

(iv) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1911 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(ix) FEATURES:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..625

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) LOCATION: 626..1582

(ix) FEATURES:

- (A) NAME/KEY: 3'UTR

20076157.024502

(B) LOCATION: 1583..1911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGTAGTCGCT CATCGACAGA CACAATCGCG TGTTCTCTCT GAATCGTCCA TTGGGTGTCA 60

GCATCCTGAT CGCGGGCGGA TGAATGGGT AATCATTAGG AACACCAAT GTCCCATGGT 120

ATTGTCCGTC CTCGTATGGT GTCTCAGGAG GACCCGTGAT CACGTAGTGC CACACCAGGA 180

TATTGTCTTC CTTTGGTGCT GCCACGATGT AGGGCGGGGG GTTCTCGGTC ATCATTTTGT 240

ACTCCTTTGA GAGCCGCTTG TACGCCTGTC TTGATGCCAT CTTGCCTACT ATTAGTTTCT 300

CACCACTTCC CGCCAAACAA TCTGCACTTT ACGAGCGCTA TCTATCCCTC GGGTCGCTCT 360

AGTTGATTAT TGGCGAAACT GATAGTTCAG GTACTTCCAT GATGCGGTCA TATCCACGTA 420

TGTGATCAG TGATCATCAG CCATGCTGCC AGCTCACGGG CCTGCCTACA CTATTGGAGG 480

CTCTGTGAGT CATGATTTAT TGCATATCAA GCCCAGATAG TCGTTGGGGA TACTACCGTT 540

GCCGCGATGA GCTCCGATAT TAAGTTGTAG CCAAAAATTT TAACGGATGA CTTCTTAACA 600

GTTATTGACG CCGCAATCCT ACGCC ATG TCG TCC AAT AGC ATA AAG CTG CTA 652
Met Ser Ser Asn Ser Ile Lys Leu Leu
1 5

GCA GGT AAC TCG CAC CCG GAC CTA GCT GAG AAG GTC TCC GTT CGC CTA 700
Ala Gly Asn Ser His Pro Asp Leu Ala Glu Lys Val Ser Val Arg Leu
10 15 20 25

GGT GTA CCA CTT TCG AAG ATT GGA GTG TAT CAC TAC TCT AAC AAA GAG 748
Gly Val Pro Leu Ser Lys Ile Gly Val Tyr His Tyr Ser Asn Lys Glu
30 35 40

ACG TCA GTT ACT ATC GGC GAA AGT ATC CGT GAT GAA GAT GTC TAC ATC 796
Thr Ser Val Thr Ile Gly Glu Ser Ile Arg Asp Glu Asp Val Tyr Ile
45 50 55

ATC CAG ACA GGA ACG GGG GAG CAG GAA ATC AAC GAC TTC CTC ATG GAA 844
Ile Gln Thr Gly Thr Gly Glu Gln Glu Ile Asn Asp Phe Leu Met Glu
60 65 70

CTG CTC ATC ATG ATC CAT GCC TGC CGG TCA GCC TCT GCG CGG AAG ATC 892
Leu Leu Ile Met Ile His Ala Cys Arg Ser Ala Ser Ala Arg Lys Ile
75 80 85

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ACA GCG GTT ATA CCA AAC TTC CCT TAC GCA AGA CAA GAC AAA AAG GAC	940
Thr Ala Val Ile Pro Asn Phe Pro Tyr Ala Arg Gln Asp Lys Lys Asp	
90 95 100 105	
AAG TCG CGA GCA CCG ATA ACT GCC AAG CTG GTG GCC AAG ATG CTA GAG	988
Lys Ser Arg Ala Pro Ile Thr Ala Lys Leu Val Ala Lys Met Leu Glu	
110 115 120	
ACC GCG GGG TGC AAC CAC GTT ATC ACG ATG GAT TTG CAC GCG TCT CAA	1036
Thr Ala Gly Cys Asn His Val Ile Thr Met Asp Leu His Ala Ser Gln	
125 130 135	
ATT CAG GGT TTC TTC CAC ATT CCA GTG GAC AAC CTA TAT GCA GAG CCG	1084
Ile Gln Gly Phe Phe His Ile Pro Val Asp Asn Leu Tyr Ala Glu Pro	
140 145 150	
AAC ATC CTG CAC TAC ATC CAA CAT AAT GTG GAC TTC CAG AAT AGT ATG	1132
Asn Ile Leu His Tyr Ile Gln His Asn Val Asp Phe Gln Asn Ser Met	
155 160 165	
TTG GTC GCG CCA GAC GCG GGG TCG GCG AAG CGC ACG TCG ACG CTT TCG	1180
Leu Val Ala Pro Asp Ala Gly Ser Ala Lys Arg Thr Ser Thr Leu Ser	
170 175 180 185	
GAC AAG CTG AAT CTC AAC TTC GCG TTG ATC CAC AAA GAA CGG CAG AAG	1228
Asp Lys Leu Asn Leu Asn Phe Ala Leu Ile His Lys Glu Arg Gln Lys	
190 195 200	
GCG AAC GAG GTC TCG CGG ATG GTG TTG GTG GGT GAT GTC GCC GAC AAG	1276
Ala Asn Glu Val Ser Arg Met Val Leu Val Gly Asp Val Ala Asp Lys	
205 210 215	
TCC TGT ATT ATT GTA GAC GAC ATG GCG GAC ACG TGC GGA ACG CTA GTG	1324
Ser Cys Ile Ile Val Asp Asp Met Ala Asp Thr Cys Gly Thr Leu Val	
220 225 230	
AAG GCC ACT GAC ACG CTG ATC GAA AAT TGT GCG AAA GAA GTG ATT GCC	1372
Lys Ala Thr Asp Thr Leu Ile Glu Asn Cys Ala Lys Glu Val Ile Ala	
235 240 245	
ATT GTG ACA CAC GGT ATA TTT TCT GGC GGC GCC CGC GAG AAG TTG CGC	1420
Ile Val Thr His Gly Ile Phe Ser Gly Gly Ala Arg Glu Lys Leu Arg	
250 255 260 265	
AAC AGC AAG CTG GCA CGG ATC GTA AGC ACA AAT ACG GTG CCA GTG GAC	1468
Asn Ser Lys Leu Ala Arg Ile Val Ser Thr Asn Thr Val Pro Val Asp	
270 275 280	

CTC AAT CTA GAT ATC TAC CAC CAA ATT GAC ATT AGT GCC ATT TTG GCC 1516
 Leu Asn Leu Asp Ile Tyr His Gln Ile Asp Ile Ser Ala Ile Leu Ala
 285 290 295

GAG GCA ATT AGA AGG CTT CAC AAC GGG GAA AGT GTG TCG TAC CTG TTC 1564
 Glu Ala Ile Arg Arg Leu His Asn Gly Glu Ser Val Ser Tyr Leu Phe
 300 305 310

AAT AAC GCT GTC ATG TAGTGCTGTC AGTGGCAGAT GCATGATCGC TGGCCTAATT 1619
 Asn Asn Ala Val Met
 315

ATCTGTGTAA GTTGATACAA TGCAGTAAAT ACAGTACATA AAACCTGAATG TTTTTCACCTT 1679

AGGGGTGCTT TGTTGTTCTG ATAGCGTGTG TGCGAATTTG GAGGTGAAAG TTGAACATCA 1739

CGTAATGAAT ACAAACAAGA TTGCACATTA GGAAAAGCGA TAAATTATTT ATTATTTGCA 1799

ACTGGCCTTT GAGCGTTTAA GCCTGAACAT TTTTGCCCTT TTGTTTGACC GTACCGTTAT 1859

CACTCGTCCT TATATATGGC TATCCTTCTC TTCCGGAAC TCTTCGAGCG TA 1911

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ser Ser Asn Ser Ile Lys Leu Leu Ala Gly Asn Ser His Pro Asp
 1 5 10 15

Leu Ala Glu Lys Val Ser Val Arg Leu Gly Val Pro Leu Ser Lys Ile
 20 25 30

Gly Val Tyr His Tyr Ser Asn Lys Glu Thr Ser Val Thr Ile Gly Glu
 35 40 45

Ser Ile Arg Asp Glu Asp Val Tyr Ile Ile Gln Thr Gly Thr Gly Glu
 50 55 60

Gln Glu Ile Asn Asp Phe Leu Met Glu Leu Leu Ile Met Ile His Ala
 65 70 75 80

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(2) INFORMATION FOR SEQ ID NO: 3:

(A) LENGTH: 5369 base pairs

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(ix) FEATURES:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..54

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) LOCATION: 55..1482

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1767..3299

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3588..4703

(ix) FEATURES:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 4704..5369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AAGCTTGACC TTGGCTGGCA CTTGAGTCGG CAGACAGGTG GACTAACCCG AGCA ATG	57
Met	
1	
GAT CGT GGT TGT AAA GGT ATC TCT TAT GTG CTC AGT GCA ATG GTT TTT	105
Asp Arg Gly Cys Lys Gly Ile Ser Tyr Val Leu Ser Ala Met Val Phe	
5 10 15	
CAC ATA ATA CCG ATT ACA TTT GAA ATA TCG ATG GTA TGT GGC ATA TTG	153
His Ile Ile Pro Ile Thr Phe Glu Ile Ser Met Val Cys Gly Ile Leu	
20 25 30	

ACA TAC CAG TTT GGT GCT TCC TTC GCT GCT ATA ACA TTC TCG ACT ATG	201
Thr Tyr Gln Phe Gly Ala Ser Phe Ala Ala Ile Thr Phe Ser Thr Met	
35 40 45	
CTT CTT TAC TCC ATC TTT ACT TTC AGA ACG ACG GCG TGG CGC ACA CGG	249
Leu Leu Tyr Ser Ile Phe Thr Phe Arg Thr Thr Ala Trp Arg Thr Arg	
50 55 60 65	
TTT AGG CGT GAT GCG AAC AAG GCT GAC AAT AAG GCC GCT AGT GTG GCA	297
Phe Arg Arg Asp Ala Asn Lys Ala Asp Asn Lys Ala Ala Ser Val Ala	
70 75 80	
TTG GAT TCC CTA ATA AAT TTT GAA GCT GTA AAG TAT TTC AAT AAC GAG	345
Leu Asp Ser Leu Ile Asn Phe Glu Ala Val Lys Tyr Phe Asn Asn Glu	
85 90 95	
AAG TAC CTT GCG GAC AAG TAT CAC ACA TCC TTG ATG AAG TAC CGG GAT	393
Lys Tyr Leu Ala Asp Lys Tyr His Thr Ser Leu Met Lys Tyr Arg Asp	
100 105 110	
TCC CAG ATA AAG GTC TCG CAA TCG CTG GCG TTT TTG AAC ACC GGC CAG	441
Ser Gln Ile Lys Val Ser Gln Ser Leu Ala Phe Leu Asn Thr Gly Gln	
115 120 125	
AAC CTA ATT TTT ACC ACT GCA CTG ACT GCA ATG ATG TAT ATG GCC TGT	489
Asn Leu Ile Phe Thr Thr Ala Leu Thr Ala Met Met Tyr Met Ala Cys	
130 135 140 145	
AAT GGT GTT ATG CAG GGC TCT CTT ACA GTG GGG GAT CTT GTG TTA ATT	537
Asn Gly Val Met Gln Gly Ser Leu Thr Val Gly Asp Leu Val Leu Ile	
150 155 160	
AAT CAA CTG GTA TTC CAG CTC TCC GTG CCA CTA AAC TTC CTT GGT AGC	585
Asn Gln Leu Val Phe Gln Leu Ser Val Pro Leu Asn Phe Leu Gly Ser	
165 170 175	
GTC TAC CGT GAT CTC AAG CAG TCT CTG ATA GAT ATG GAA TCT TTA TTT	633
Val Tyr Arg Asp Leu Lys Gln Ser Leu Ile Asp Met Glu Ser Leu Phe	
180 185 190	
AAA CTG CAA AAA AAT CAG GTC ACA ATT AAG AAC TCC CCA AAT GCC CAG	681
Lys Leu Gln Lys Asn Gln Val Thr Ile Lys Asn Ser Pro Asn Ala Gln	
195 200 205	
AAC CTA CCA ATA CAC AAA CCG TTG GAT ATT CGC TTT GAA AAT GTT ACG	729
Asn Leu Pro Ile His Lys Pro Leu Asp Ile Arg Phe Glu Asn Val Thr	
210 215 220 225	

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TTT GGC TAT GAC CCG GAG CGG CGT ATA TTG AAC AAT GTT TCG TTT ACC	777
Phe Gly Tyr Asp Pro Glu Arg Arg Ile Leu Asn Asn Val Ser Phe Thr	
230 235 240	
ATC CCA GCT GGA ATG AAG ACT GCC ATA GTA GGC CCA TCG GGC TCG GGG	825
Ile Pro Ala Gly Met Lys Thr Ala Ile Val Gly Pro Ser Gly Ser Gly	
245 250 255	
AAG TCC ACC ATT TTG AAG CTC GTA TTT AGA TTC TAT GAG CCC GAG CAA	873
Lys Ser Thr Ile Leu Lys Leu Val Phe Arg Phe Tyr Glu Pro Glu Gln	
260 265 270	
GGT CGT ATC CTA GTT GGC GGC ACA GAT ATC CGC GAT TTA GAC TTG CTT	921
Gly Arg Ile Leu Val Gly Gly Thr Asp Ile Arg Asp Leu Asp Leu Leu	
275 280 285	
TCT TTA CGG AAG GCT ATC GGT GTC GTG CCC CAA GAT ACT CCT CTC TTC	969
Ser Leu Arg Lys Ala Ile Gly Val Val Pro Gln Asp Thr Pro Leu Phe	
290 295 300 305	
AAT GAC ACA ATC TGG GAG AAT GTT AAA TTC GGC AAT ATC AGT TCC TCT	1017
Asn Asp Thr Ile Trp Glu Asn Val Lys Phe Gly Asn Ile Ser Ser Ser	
310 315 320	
GAC GAT GAG ATT CTC AGG GCC ATA GAA AAA GCT CAA CTC ACG AAG CTA	1065
Asp Asp Glu Ile Leu Arg Ala Ile Glu Lys Ala Gln Leu Thr Lys Leu	
325 330 335	
CTC CAG AAC CTA CCA AAG GGC GCT TCC ACC GTT GTA GGG GAG CGC GGT	1113
Leu Gln Asn Leu Pro Lys Gly Ala Ser Thr Val Val Gly Glu Arg Gly	
340 345 350	
TTG ATG ATC AGC GGA GGT GAG AAA CAA AGG CTT GCT ATT GCT CGT GTG	1161
Leu Met Ile Ser Gly Gly Glu Lys Gln Arg Leu Ala Ile Ala Arg Val	
355 360 365	
CTT TTG AAG GAC GCT CCG CTG ATG TTT TTC GAC GAG GCT ACA AGT GCT	1209
Leu Leu Lys Asp Ala Pro Leu Met Phe Phe Asp Glu Ala Thr Ser Ala	
370 375 380 385	
CTG GAT ACA CAC ACA GAG CAG GCA CTC TTG CAC ACC ATT CAG CAG AAC	1257
Leu Asp Thr His Thr Glu Gln Ala Leu Leu His Thr Ile Gln Gln Asn	
390 395 400	
TTT TCT TCC AAT TCA AAG ACG AGC GTT TAC GTT GCC CAT AGA CTG CGC	1305
Phe Ser Ser Asn Ser Lys Thr Ser Val Tyr Val Ala His Arg Leu Arg	
405 410 415	

ACA ATC GCT GAT GCA GAT AAG ATC ATT GTT CTT GAA CAA GGT TCT GTC 1353
 Thr Ile Ala Asp Ala Asp Lys Ile Ile Val Leu Glu Gln Gly Ser Val
 420 425 430

CGC GAA GAG GGC ACA CAC AGC TCG CTG TTA GCG TCA CAA GGA TCC CTA 1401
 Arg Glu Glu Gly Thr His Ser Ser Leu Leu Ala Ser Gln Gly Ser Leu
 435 440 445

TAC CGG GGT CTG TGG GAT ATT CAG GAA AAC CTA ACG CTT CCG GAA CGG 1449
 Tyr Arg Gly Leu Trp Asp Ile Gln Glu Asn Leu Thr Leu Pro Glu Arg
 450 455 460 465

CCT GAG CAG TCA ACC GGA TCT CAG CAT GCA TAGACGTCTG ACTAGAGATT 1499
 Pro Glu Gln Ser Thr Gly Ser Gln His Ala
 470 475

ATATAATAAC CCTCGAGCCA AAATTATACG GCGCTAACAA GTAAAAATTT TAGTTACTTT 1559

TCTGACTTCT CTACGCTGAC TTCTCTACCC TTCTAACATA GTTAATTGAA GTAGTGGTTA 1619

ATGACGACTG CATTTTATTA TTGTCCACTT TGCATTAGAA GTACTAGTGC TTAAGCGCTC 1679

TTTAGGCCGC TTTCTTCTTC TTTGTCAGGC CGCAAGGTAA AGGAAGCACC AACGGATTGC 1739

TACCGCTGCT ATTCCTGCTC TCTCAAG ATG TGT GGC ATA TTA GGC GTT GTG 1790
 Met Cys Gly Ile Leu Gly Val Val
 1 5

CTA GCC GAT CAG TCG AAG GTG GTC GCC CCT GAG TTG TTT GAT GGC TCA 1838
 Leu Ala Asp Gln Ser Lys Val Val Ala Pro Glu Leu Phe Asp Gly Ser
 10 15 20

CTG TTC TTA CAG CAT CGC GGT CAA GAT GCT GCC GGG ATT GCT ACG TGC 1886
 Leu Phe Leu Gln His Arg Gly Gln Asp Ala Ala Gly Ile Ala Thr Cys
 25 30 35 40

GGC CCC GGT GGG CGC TTG TAC CAA TGT AAG GGC AAT GGT ATG GCA CGG 1934
 Gly Pro Gly Gly Arg Leu Tyr Gln Cys Lys Gly Asn Gly Met Ala Arg
 45 50 55

GAC GTG TTC ACG CAA GCT CGG ATG TCA GGG TTG GTT GGC TCT ATG GGG 1982
 Asp Val Phe Thr Gln Ala Arg Met Ser Gly Leu Val Gly Ser Met Gly
 60 65 70

ATT GCA CAC CTG AGA TAT CCC ACT GCA GGC TCC AGT GCG AAC TCA GAA 2030
 Ile Ala His Leu Arg Tyr Pro Thr Ala Gly Ser Ser Ala Asn Ser Glu
 75 80 85

GCG CAG CCA TTC TAT GTG AAT AGT CCC TAC GGA ATT TGC ATG AGT CAT	2078
Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly Ile Cys Met Ser His	
90 95 100	
AAT GGT AAT CTG GTG AAC ACG ATG TCT CTA CGT AGA TAT CTT GAT GAA	2126
Asn Gly Asn Leu Val Asn Thr Met Ser Leu Arg Arg Tyr Leu Asp Glu	
105 110 115 120	
GAC GTT CAC CGT CAT ATT AAC ACG GAC AGC GAT TCT GAG CTA CTG CTT	2174
Asp Val His Arg His Ile Asn Thr Asp Ser Asp Ser Glu Leu Leu Leu	
125 130 135	
AAT ATA TTT GCC GCG GAG CTG GAA AAG TAC AAC AAA TAT CGT GTG AAC	2222
Asn Ile Phe Ala Ala Glu Leu Glu Lys Tyr Asn Lys Tyr Arg Val Asn	
140 145 150	
AAC GAT GAT ATA TTT TGT GCT CTA GAG GGT GTT TAC AAA CGT TGT CGC	2270
Asn Asp Asp Ile Phe Cys Ala Leu Glu Gly Val Tyr Lys Arg Cys Arg	
155 160 165	
GGT GGC TAT GCT TGT GTT GGC ATG TTG GCG GGA TAT GGA TTG TTT GGT	2318
Gly Gly Tyr Ala Cys Val Gly Met Leu Ala Gly Tyr Gly Leu Phe Gly	
170 175 180	
TTC CGG GAC CCC AAT GGG ATC AGG CCG CTA TTG TTT GGT GAG CGC GTC	2366
Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Leu Phe Gly Glu Arg Val	
185 190 195 200	
AAC GAT GAC GGC ACC ATG GAC TAC ATG CTA GCG TCC GAA AGT GTC GTT	2414
Asn Asp Asp Gly Thr Met Asp Tyr Met Leu Ala Ser Glu Ser Val Val	
205 210 215	
CTT AAG GCC CAC CGC TTC CAA AAC ATA CGT GAT ATT CTT CCC GGC CAA	2462
Leu Lys Ala His Arg Phe Gln Asn Ile Arg Asp Ile Leu Pro Gly Gln	
220 225 230	
GCC GTC ATT ATC CCT AAA ACG TGC GGC TCC AGT CCA CCA GAG TTC CGG	2510
Ala Val Ile Ile Pro Lys Thr Cys Gly Ser Ser Pro Pro Glu Phe Arg	
235 240 245	
CAG GTA GTG CCA ATT GAG GCC TAC AAA CCG GAC TTG TTT GAG TAC GTG	2558
Gln Val Val Pro Ile Glu Ala Tyr Lys Pro Asp Leu Phe Glu Tyr Val	
250 255 260	
TAT TTC GCT CGT GCT GAC AGC GTT CTG GAC GGT ATT TCC GTT TAC CAT	2606
Tyr Phe Ala Arg Ala Asp Ser Val Leu Asp Gly Ile Ser Val Tyr His	
265 270 275 280	

ACA CGC CTG TTG ATG GGT ATC AAA CTT GCC GAG AAC ATC AAA AAA CAG 2654
 Thr Arg Leu Leu Met Gly Ile Lys Leu Ala Glu Asn Ile Lys Lys Gln
 285 290 295

ATC GAT CTG GAC GAA ATT GAC GTT GTT GTA TCT GTT CCT GAC ACT GCA 2702
 Ile Asp Leu Asp Glu Ile Asp Val Val Val Ser Val Pro Asp Thr Ala
 300 305 310

CGT ACC TGT GCA TTG GAG TGT GCC AAC CAT TTA AAC AAA CCT TAT CGC 2750
 Arg Thr Cys Ala Leu Glu Cys Ala Asn His Leu Asn Lys Pro Tyr Arg
 315 320 325

GAA GGA TTT GTC AAG AAC AGA TAT GTT GGA AGA ACA TTT ATC ATG CCA 2798
 Glu Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile Met Pro
 330 335 340

AAC CAA AAA GAG CGA GTA TCT TCT GTG CGC CGC AAG TTG AAC CCA ATG 2846
 Asn Gln Lys Glu Arg Val Ser Ser Val Arg Arg Lys Leu Asn Pro Met
 345 350 355 360

AAC TCA GAA TTT AAA GAC AAG CGC GTG CTG ATT GTC GAT GAT TCC ATT 2894
 Asn Ser Glu Phe Lys Asp Lys Arg Val Leu Ile Val Asp Asp Ser Ile
 365 370 375

GTG CGA GGT ACC ACT TCC AAA GAG ATT GTT AAC ATG GCG AAG GAA TCC 2942
 Val Arg Gly Thr Thr Ser Lys Glu Ile Val Asn Met Ala Lys Glu Ser
 380 385 390

GGT GCT GCC AAG GTC TAC TTT GCC TCT GCA GCG CCA GCA ATT CGT TTC 2990
 Gly Ala Ala Lys Val Tyr Phe Ala Ser Ala Ala Pro Ala Ile Arg Phe
 395 400 405

AAT CAC ATC TAC GGG ATT GAC CTA GCA GAT ACT AAG CAG CTT GTC GCC 3038
 Asn His Ile Tyr Gly Ile Asp Leu Ala Asp Thr Lys Gln Leu Val Ala
 410 415 420

TAC AAC AGA ACT GTT GAA GAA ATC ACT GCG GAG CTG GGC TGT GAC CGC 3086
 Tyr Asn Arg Thr Val Glu Glu Ile Thr Ala Glu Leu Gly Cys Asp Arg
 425 430 435 440

GTC ATC TAT CAA TCT TTG GAT GAC CTC ATC GAC TGT TGC AAG ACA GAC 3134
 Val Ile Tyr Gln Ser Leu Asp Asp Leu Ile Asp Cys Cys Lys Thr Asp
 445 450 455

ATC ATC TCA GAA TTT GAA GTT GGA GTT TTC ACT GGT AAC TAC GTT ACA 3182
 Ile Ile Ser Glu Phe Glu Val Gly Val Phe Thr Gly Asn Tyr Val Thr
 460 465 470

GGT GTT GAG GAT GTG TAC TTG CAG GAA TTA GAA CGT TGC CGC GCT CTT 3230
 Gly Val Glu Asp Val Tyr Leu Gln Glu Leu Glu Arg Cys Arg Ala Leu
 475 480 485

AAT AAC TCG AAT AAG GGT GAA GCG AAG GCC GAG GTT GAT ATT GGT CTC 3278
 Asn Asn Ser Asn Lys Gly Glu Ala Lys Ala Glu Val Asp Ile Gly Leu
 490 495 500

TAC AAT TCT GCC GAC TAT TAGCGGCGCC GTTGCCGGCA TCCGGCCCCA 3326
 Tyr Asn Ser Ala Asp Tyr
 505 510

TATATAGACT CATCGGGACC TAAAATAAGC CTTTACAGAT CATTATCTAC AAATATAGAT 3386

ACCATTAATA GCCTGACTTT CCACTTACTC CTAGCACACC CCGTTGTATC CCTGTGCTTG 3446

CTTTCTTAAA TGCCGTTGGT TAGGCTTTGG ACTTAGCGTC CCGCCCATTT TCTAGCATGT 3506

GCAGATCTAG CAAATTTGGC CTAAGACAAG AAGATCCATT CGGCACCCAC ATCCTGGAGC 3566

CAGCACACAG TGGACCCAGA C ATG AGC AGC GGC AAT ATA TGG AAG CAA TTG 3617
 Met Ser Ser Gly Asn Ile Trp Lys Gln Leu
 1 5 10

CTA GAG GAG AAT AGC GAA CAG CTG GAC CAG TCC ACT ACG GAG ACT TAC 3665
 Leu Glu Glu Asn Ser Glu Gln Leu Asp Gln Ser Thr Thr Glu Thr Tyr
 15 20 25

GTG GTA TGC TGC GAG AAC GAA GAT TCC CTT AAC CAG TTT TTG CAA CAA 3713
 Val Val Cys Cys Glu Asn Glu Asp Ser Leu Asn Gln Phe Leu Gln Gln
 30 35 40

TGT TGG CAG ATT GAC GAG GGC GAG AAG GTG ACC AAC CTG GAG CCG TTG 3761
 Cys Trp Gln Ile Asp Glu Gly Glu Lys Val Thr Asn Leu Glu Pro Leu
 45 50 55

GGA TTC TTT ACA AAG GTG GTT TCG CGC GAC GAA GAG AAC CTC CGG CTC 3809
 Gly Phe Phe Thr Lys Val Val Ser Arg Asp Glu Glu Asn Leu Arg Leu
 60 65 70

AAC GTA TAC TAT GCC AAG AGC CCA CTG GAT GCA CAG ACG CTG CAG TTT 3857
 Asn Val Tyr Tyr Ala Lys Ser Pro Leu Asp Ala Gln Thr Leu Gln Phe
 75 80 85 90

CTG GGC GTG TTC CTG CGC CAA ATG GAA ACC TCA CAA ATA CGT TGG ATC 3905
 Leu Gly Val Phe Leu Arg Gln Met Glu Thr Ser Gln Ile Arg Trp Ile
 95 100 105

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TTC	CTA	CTG	GAC	TGG	CTG	CTA	GAC	GAT	AAA	CGA	TTA	TGG	CTA	CGT	CAA	3953
Phe	Leu	Leu	Asp	Trp	Leu	Leu	Asp	Asp	Lys	Arg	Leu	Trp	Leu	Arg	Gln	
			110					115						120		
CTG	CGG	AAC	TCG	TGG	GCC	GCC	TTG	GAG	GAA	GCG	CAG	GTG	GCA	CCC	TTT	4001
Leu	Arg	Asn	Ser	Trp	Ala	Ala	Leu	Glu	Glu	Ala	Gln	Val	Ala	Pro	Phe	
			125				130							135		
CCA	GGT	GGC	GCT	GTG	GTG	GTG	GTC	CTC	AAC	CCG	AGT	CAC	GTG	ACA	CAA	4049
Pro	Gly	Gly	Ala	Val	Val	Val	Val	Leu	Asn	Pro	Ser	His	Val	Thr	Gln	
			140				145							150		
CTG	GAG	CGA	AAC	ACG	ATG	GTT	TGG	AAC	TCC	CGC	CGT	CTG	GAC	CTG	GTA	4097
Leu	Glu	Arg	Asn	Thr	Met	Val	Trp	Asn	Ser	Arg	Arg	Leu	Asp	Leu	Val	
						160				165					170	
CAC	CAG	ACA	CTG	CGA	GCT	GCA	TGC	CTC	AAC	ACC	GGC	TCG	GCG	CTA	GTT	4145
His	Gln	Thr	Leu	Arg	Ala	Ala	Cys	Leu	Asn	Thr	Gly	Ser	Ala	Leu	Val	
						175				180					185	
ACA	CTT	GAT	CCT	AAT	ACT	GCG	CGC	GAA	GAC	GTC	ATG	CAC	ATA	TGT	GCG	4193
Thr	Leu	Asp	Pro	Asn	Thr	Ala	Arg	Glu	Asp	Val	Met	His	Ile	Cys	Ala	
						190				195				200		
CTG	CTT	GCG	GGG	CTG	CCT	ACA	TCC	CGT	CCC	GTC	GCG	ATG	CTA	AGC	CTG	4241
Leu	Leu	Ala	Gly	Leu	Pro	Thr	Ser	Arg	Pro	Val	Ala	Met	Leu	Ser	Leu	
			205					210						215		
CAA	AGT	CTA	TTC	ATC	CCC	CAC	GGT	GCA	GAT	TCC	ATC	GGC	AAG	ATC	TGC	4289
Gln	Ser	Leu	Phe	Ile	Pro	His	Gly	Ala	Asp	Ser	Ile	Gly	Lys	Ile	Cys	
			220				225							230		
ACC	ATC	GCG	CCC	GAG	TTC	CCT	GTT	GCT	ACG	GTG	TTC	GAC	AAC	GAT	TTT	4337
Thr	Ile	Ala	Pro	Glu	Phe	Pro	Val	Ala	Thr	Val	Phe	Asp	Asn	Asp	Phe	
						240				245					250	
GTG	AGC	TCG	ACA	TTC	GAG	GCC	GCA	ATT	GCT	CCA	GAA	CTT	ACT	CCA	GGA	4385
Val	Ser	Ser	Thr	Phe	Glu	Ala	Ala	Ile	Ala	Pro	Glu	Leu	Thr	Pro	Gly	
						255				260					265	
CCA	CGT	GTG	CCA	TCT	GAC	CAC	CCA	TGG	CTA	ACA	GAG	CCT	ACC	AAC	CCC	4433
Pro	Arg	Val	Pro	Ser	Asp	His	Pro	Trp	Leu	Thr	Glu	Pro	Thr	Asn	Pro	
						270				275				280		
CCT	TCG	GAG	GCA	ACC	GCT	TGG	CAT	TTC	GAT	CTC	CAA	GGT	CGC	CTC	GCT	4481
Pro	Ser	Glu	Ala	Thr	Ala	Trp	His	Phe	Asp	Leu	Gln	Gly	Arg	Leu	Ala	
						285				290				295		

ACC CTA TAC CGG CAT CTT GGT GAC TCT AAC AAG GCC ATA TCT GTT ACT 4529
 Thr Leu Tyr Arg His Leu Gly Asp Ser Asn Lys Ala Ile Ser Val Thr
 300 305 310

CAG CAC CGC TTC CAC AAG CCC CGC TCG GAA GAT TAT GCA TAC GAA TTC 4577
 Gln His Arg Phe His Lys Pro Arg Ser Glu Asp Tyr Ala Tyr Glu Phe
 315 320 325 330

GAG CTG CCG TCT AAG CAC CCT ACA ATA CGT GAC CTC ATA CGC TCT GCC 4625
 Glu Leu Pro Ser Lys His Pro Thr Ile Arg Asp Leu Ile Arg Ser Ala
 335 340 345

GCA GCC GAC TCA CCG AAC GAC GTC GCT GAC TCC ATC GAT GGG CTT ATG 4673
 Ala Ala Asp Ser Pro Asn Asp Val Ala Asp Ser Ile Asp Gly Leu Met
 350 355 360

GAT GGT ATC GTA CAA AGG AAT GTT CAT TGACGTCGAC ACAAAAATTT 4720
 Asp Gly Ile Val Gln Arg Asn Val His
 365 370

TGTTACTGTT CTCTCGAGAA CTATTCTCAT CCAGTACTGA CATATTAGAA GGCGAAGTGA 4780

ACTAGGATTT ATATAAAGTA GCCTTCAGGC AATTGCACAG GGTCTATTGA GTCGCTGCCG 4840

TTCACGAGAG AGCCCAATAT ATCGAGGACT AATTGGTCAC TTTTGTTTTG CTATACTCAC 4900

CCTGTATTTG CTAATCATTT ATCCGCTTTG TCCAAGTGGT TGCGAAGATA TCGAGCCAGA 4960

ACATTAGAAT CTGGTTTGCC GCATCCTAGA GCTGTCTCCA AGCCAGTTGA ACCGTTGCGG 5020

GAGATTACCG CAGCCGGTTT GATCAGAGTA CTGGTGACTG CCAGCACCCA CGTTTGTGAC 5080

TTATAAATAT ACGCCCTGTG GAGCCATAGC CATTGGCATA AAGAGAAGAG CACCCCGTGC 5140

CACGATGCAG ACACTTCCGG TGTACCCAGC GTCACAGACT GCGTCGCCTA CGAAGCGTGA 5200

ACTTGCAGCG GCGCCCTCGG TGCCGCAGGA CGGCGCCCGG CTGCCTGCGC AGCTCACTTT 5260

AGTGACGCCC CCAGAACCTG ATATCCAGAA GAAGTCAGTG CGATCTCAGG TCGCGCGTTT 5320

AAGCATCTCG GAGACAGATG TAGTGAAGAG TGATATCGTG GCTAAGCTT 5369

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Asp Arg Gly Cys Lys Gly Ile Ser Tyr Val Leu Ser Ala Met Val
 1 5 10 15
 Phe His Ile Ile Pro Ile Thr Phe Glu Ile Ser Met Val Cys Gly Ile
 20 25 30
 Leu Thr Tyr Gln Phe Gly Ala Ser Phe Ala Ala Ile Thr Phe Ser Thr
 35 40 45
 Met Leu Leu Tyr Ser Ile Phe Thr Phe Arg Thr Thr Ala Trp Arg Thr
 50 55 60
 Arg Phe Arg Arg Asp Ala Asn Lys Ala Asp Asn Lys Ala Ala Ser Val
 65 70 75 80
 Ala Leu Asp Ser Leu Ile Asn Phe Glu Ala Val Lys Tyr Phe Asn Asn
 85 90 95
 Glu Lys Tyr Leu Ala Asp Lys Tyr His Thr Ser Leu Met Lys Tyr Arg
 100 105 110
 Asp Ser Gln Ile Lys Val Ser Gln Ser Leu Ala Phe Leu Asn Thr Gly
 115 120 125
 Gln Asn Leu Ile Phe Thr Thr Ala Leu Thr Ala Met Met Tyr Met Ala
 130 135 140
 Cys Asn Gly Val Met Gln Gly Ser Leu Thr Val Gly Asp Leu Val Leu
 145 150 155 160
 Ile Asn Gln Leu Val Phe Gln Leu Ser Val Pro Leu Asn Phe Leu Gly
 165 170 175
 Ser Val Tyr Arg Asp Leu Lys Gln Ser Leu Ile Asp Met Glu Ser Leu
 180 185 190
 Phe Lys Leu Gln Lys Asn Gln Val Thr Ile Lys Asn Ser Pro Asn Ala
 195 200 205
 Gln Asn Leu Pro Ile His Lys Pro Leu Asp Ile Arg Phe Glu Asn Val
 210 215 220
 Thr Phe Gly Tyr Asp Pro Glu Arg Arg Ile Leu Asn Asn Val Ser Phe
 225 230 235 240

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Thr Ile Pro Ala Gly Met Lys Thr Ala Ile Val Gly Pro Ser Gly Ser
 245 250 255
 Gly Lys Ser Thr Ile Leu Lys Leu Val Phe Arg Phe Tyr Glu Pro Glu
 260 265 270
 Gln Gly Arg Ile Leu Val Gly Gly Thr Asp Ile Arg Asp Leu Asp Leu
 275 280 285
 Leu Ser Leu Arg Lys Ala Ile Gly Val Val Pro Gln Asp Thr Pro Leu
 290 295 300
 Phe Asn Asp Thr Ile Trp Glu Asn Val Lys Phe Gly Asn Ile Ser Ser
 305 310 315 320
 Ser Asp Asp Glu Ile Leu Arg Ala Ile Glu Lys Ala Gln Leu Thr Lys
 325 330 335
 Leu Leu Gln Asn Leu Pro Lys Gly Ala Ser Thr Val Val Gly Glu Arg
 340 345 350
 Gly Leu Met Ile Ser Gly Gly Glu Lys Gln Arg Leu Ala Ile Ala Arg
 355 360 365
 Val Leu Leu Lys Asp Ala Pro Leu Met Phe Phe Asp Glu Ala Thr Ser
 370 375 380
 Ala Leu Asp Thr His Thr Glu Gln Ala Leu Leu His Thr Ile Gln Gln
 385 390 395 400
 Asn Phe Ser Ser Asn Ser Lys Thr Ser Val Tyr Val Ala His Arg Leu
 405 410 415
 Arg Thr Ile Ala Asp Ala Asp Lys Ile Ile Val Leu Glu Gln Gly Ser
 420 425 430
 Val Arg Glu Glu Gly Thr His Ser Ser Leu Leu Ala Ser Gln Gly Ser
 435 440 445
 Leu Tyr Arg Gly Leu Trp Asp Ile Gln Glu Asn Leu Thr Leu Pro Glu
 450 455 460
 Arg Pro Glu Gln Ser Thr Gly Ser Gln His Ala
 465 470 475

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 510 Amino acids

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(B) TYPE: Amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Cys Gly Ile Leu Gly Val Val Leu Ala Asp Gln Ser Lys Val Val
1 5 10 15

Ala Pro Glu Leu Phe Asp Gly Ser Leu Phe Leu Gln His Arg Gly Gln
20 25 30

Asp Ala Ala Gly Ile Ala Thr Cys Gly Pro Gly Gly Arg Leu Tyr Gln
35 40 45

Cys Lys Gly Asn Gly Met Ala Arg Asp Val Phe Thr Gln Ala Arg Met
50 55 60

Ser Gly Leu Val Gly Ser Met Gly Ile Ala His Leu Arg Tyr Pro Thr
65 70 75 80

Ala Gly Ser Ser Ala Asn Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser
85 90 95

Pro Tyr Gly Ile Cys Met Ser His Asn Gly Asn Leu Val Asn Thr Met
100 105 110

Ser Leu Arg Arg Tyr Leu Asp Glu Asp Val His Arg His Ile Asn Thr
115 120 125

Asp Ser Asp Ser Glu Leu Leu Leu Asn Ile Phe Ala Ala Glu Leu Glu
130 135 140

Lys Tyr Asn Lys Tyr Arg Val Asn Asn Asp Asp Ile Phe Cys Ala Leu
145 150 155 160

Glu Gly Val Tyr Lys Arg Cys Arg Gly Gly Tyr Ala Cys Val Gly Met
165 170 175

Leu Ala Gly Tyr Gly Leu Phe Gly Phe Arg Asp Pro Asn Gly Ile Arg
180 185 190

Pro Leu Leu Phe Gly Glu Arg Val Asn Asp Asp Gly Thr Met Asp Tyr
195 200 205

Met Leu Ala Ser Glu Ser Val Val Leu Lys Ala His Arg Phe Gln Asn
210 215 220

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Ile Arg Asp Ile Leu Pro Gly Gln Ala Val Ile Ile Pro Lys Thr Cys
 225 230 235 240
 Gly Ser Ser Pro Pro Glu Phe Arg Gln Val Val Pro Ile Glu Ala Tyr
 245 250 255
 Lys Pro Asp Leu Phe Glu Tyr Val Tyr Phe Ala Arg Ala Asp Ser Val
 260 265 270
 Leu Asp Gly Ile Ser Val Tyr His Thr Arg Leu Leu Met Gly Ile Lys
 275 280 285
 Leu Ala Glu Asn Ile Lys Lys Gln Ile Asp Leu Asp Glu Ile Asp Val
 290 295 300
 Val Val Ser Val Pro Asp Thr Ala Arg Thr Cys Ala Leu Glu Cys Ala
 305 310 315 320
 Asn His Leu Asn Lys Pro Tyr Arg Glu Gly Phe Val Lys Asn Arg Tyr
 325 330 335
 Val Gly Arg Thr Phe Ile Met Pro Asn Gln Lys Glu Arg Val Ser Ser
 340 345 350
 Val Arg Arg Lys Leu Asn Pro Met Asn Ser Glu Phe Lys Asp Lys Arg
 355 360 365
 Val Leu Ile Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Lys Glu
 370 375 380
 Ile Val Asn Met Ala Lys Glu Ser Gly Ala Ala Lys Val Tyr Phe Ala
 385 390 395 400
 Ser Ala Ala Pro Ala Ile Arg Phe Asn His Ile Tyr Gly Ile Asp Leu
 405 410 415
 Ala Asp Thr Lys Gln Leu Val Ala Tyr Asn Arg Thr Val Glu Glu Ile
 420 425 430
 Thr Ala Glu Leu Gly Cys Asp Arg Val Ile Tyr Gln Ser Leu Asp Asp
 435 440 445
 Leu Ile Asp Cys Cys Lys Thr Asp Ile Ile Ser Glu Phe Glu Val Gly
 450 455 460
 Val Phe Thr Gly Asn Tyr Val Thr Gly Val Glu Asp Val Tyr Leu Gln
 465 470 475 480
 Glu Leu Glu Arg Cys Arg Ala Leu Asn Asn Ser Asn Lys Gly Glu Ala
 485 490 495

205T20 43T9200T
 100643 024502

Lys Ala Glu Val Asp Ile Gly Leu Tyr Asn Ser Ala Asp Tyr
 500 505 510

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ser Ser Gly Asn Ile Trp Lys Gln Leu Leu Glu Glu Asn Ser Glu
 1 5 10 15

Gln Leu Asp Gln Ser Thr Thr Glu Thr Tyr Val Val Cys Cys Glu Asn
 20 25 30

Glu Asp Ser Leu Asn Gln Phe Leu Gln Gln Cys Trp Gln Ile Asp Glu
 35 40 45

Gly Glu Lys Val Thr Asn Leu Glu Pro Leu Gly Phe Phe Thr Lys Val
 50 55 60

Val Ser Arg Asp Glu Glu Asn Leu Arg Leu Asn Val Tyr Tyr Ala Lys
 65 70 75 80

Ser Pro Leu Asp Ala Gln Thr Leu Gln Phe Leu Gly Val Phe Leu Arg
 85 90 95

Gln Met Glu Thr Ser Gln Ile Arg Trp Ile Phe Leu Leu Asp Trp Leu
 100 105 110

Leu Asp Asp Lys Arg Leu Trp Leu Arg Gln Leu Arg Asn Ser Trp Ala
 115 120 125

Ala Leu Glu Glu Ala Gln Val Ala Pro Phe Pro Gly Gly Ala Val Val
 130 135 140

Val Val Leu Asn Pro Ser His Val Thr Gln Leu Glu Arg Asn Thr Met
 145 150 155 160

Val Trp Asn Ser Arg Arg Leu Asp Leu Val His Gln Thr Leu Arg Ala
 165 170 175

Ala Cys Leu Asn Thr Gly Ser Ala Leu Val Thr Leu Asp Pro Asn Thr
 180 185 190

Ala Arg Glu Asp Val Met His Ile Cys Ala Leu Leu Ala Gly Leu Pro
 195 200 205

Thr Ser Arg Pro Val Ala Met Leu Ser Leu Gln Ser Leu Phe Ile Pro
 210 215 220

His Gly Ala Asp Ser Ile Gly Lys Ile Cys Thr Ile Ala Pro Glu Phe
 225 230 235 240

Pro Val Ala Thr Val Phe Asp Asn Asp Phe Val Ser Ser Thr Phe Glu
 245 250 255

Ala Ala Ile Ala Pro Glu Leu Thr Pro Gly Pro Arg Val Pro Ser Asp
 260 265 270

His Pro Trp Leu Thr Glu Pro Thr Asn Pro Pro Ser Glu Ala Thr Ala
 275 280 285

Trp His Phe Asp Leu Gln Gly Arg Leu Ala Thr Leu Tyr Arg His Leu
 290 295 300

Gly Asp Ser Asn Lys Ala Ile Ser Val Thr Gln His Arg Phe His Lys
 305 310 315 320

Pro Arg Ser Glu Asp Tyr Ala Tyr Glu Phe Glu Leu Pro Ser Lys His
 325 330 335

Pro Thr Ile Arg Asp Leu Ile Arg Ser Ala Ala Ala Asp Ser Pro Asn
 340 345 350

Asp Val Ala Asp Ser Ile Asp Gly Leu Met Asp Gly Ile Val Gln Arg
 355 360 365

Asn Val His
 370

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3616 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(ix) FEATURES:

(A) NAME/KEY: 5'UTR

(B) LOCATION: 1..863

(ix) FEATURES:

(A) NAME/KEY: CDS

(B) LOCATION: 864..1316

(ix) FEATURES:

(A) NAME/KEY: intron

(B) LOCATION: 1317..1477

(ix) FEATURES:

(A) NAME/KEY: CDS

(B) LOCATION 1478..2592

(ix) FEATURES:

(A) NAME/KEY: 3'UTR

(B) LOCATION: 2593..3616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGGCCCCGGTG CCAGCTCGCC AGGTGCGGAC TCGCGCTCGG GCTGTGGGCG CTCTACCTGC	60
TGCTGCTCGG CAGCTGCCTG ACGCGCGCGT ACGAGCTGTC GGATCTCGAA AACCTGGAAT	120
CCGATTACTA CAGCTACGTG CTGGATGTGA ACTTCGCGCT GCTGAGCGCC ATGAGCGCGA	180
CCGGCCTCGC GATGGGCGCC GTGAGCGGCT CCCTCGGGAG CGCGCCGGTG CTCGCGCAGT	240
GGCCGGCAGC GATCTGGGCC GTGCGCTTCC TGCGCGCCGC GGGCTATGTC GCGATAGTCC	300
TAATCCTGCC GTTCTGTCC GTCGTCGCAT TCCTGCAGCC GCTCTGCGAG CGCGCGCTGG	360
CGCTGTTCCC GTTTGTGCGC GCGTGGGGCA TGGACGGCGT GTTCAACTTC CTGCTGCTCT	420
CCGCCGTGCT CTGGACTGTA TTCCTGGCCG TTCGCCTGCT CCGCGCCGTC TACAGACTGC	480
TGCGCTGGCT GGTCCGTCTT TTGGTCCGCC TGGCACGCCT GCTGCTGCGA GGCGCCCGTC	540
GGACGCCTGC GGCGGCCCCC GAGGAGCCCCG TCTAGCGTGC GCGCGTTCTA GGCCCCTGAC	600
AGCTCCTACC TGGTGCTGGC CGCCGGTAGG GCTCGCATCG TGCGGCGCAG GCCCATTTGCT	660

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TTTTGGCCCC CGCTGGATCA TCGTTTCTTT TACGTGAAAA GTTTCAGCG ATGAGCTGCA	720
GTATAAATAG GTTTTCTAGA TGCGCCAAAT CCCAGCTGGG TTTACCGGCG TCTGTTCGGG	780
ATAGTTACTT GATGGATGGG TCAACTTGAG AGCTTGGGTT TAGTGTGAC TCCTTCTCTT	840
CATAGCACGC CGAACAAAGC GCA ATG ACT TAC AGA GAC GCA GCC ACG GCA	890
Met Thr Tyr Arg Asp Ala Ala Thr Ala	
1 5	
CTG GAG CAC CTG GCG ACG TAC GCC GAG AAG GAC GGG CTG TCC GTG GAG	938
Leu Glu His Leu Ala Thr Tyr Ala Glu Lys Asp Gly Leu Ser Val Glu	
10 15 20 25	
CAG TTG ATG GAC TCC AAG ACG CGG GGC GGG TTG ACG TAC AAC GAC TTC	986
Gln Leu Met Asp Ser Lys Thr Arg Gly Gly Leu Thr Tyr Asn Asp Phe	
30 35 40	
CTG GTC TTG CCG GGC AAG ATC GAC TTC CCA TCG TCG GAG GTG GTG CTG	1034
Leu Val Leu Pro Gly Lys Ile Asp Phe Pro Ser Ser Glu Val Val Leu	
45 50 55	
TCG TCG CGC CTG ACC AAG AAG ATC ACC TTG AAC GCG CCG TTT GTG TCG	1082
Ser Ser Arg Leu Thr Lys Lys Ile Thr Leu Asn Ala Pro Phe Val Ser	
60 65 70	
TCG CCG ATG GAC ACG GTG ACG GAG GCC GAC ATG GCG ATC CAC ATG GCG	1130
Ser Pro Met Asp Thr Val Thr Glu Ala Asp Met Ala Ile His Met Ala	
75 80 85	
CTC CTG GGC GGC ATC GGG ATC ATC CAC CAC AAC TGC ACT GCG GAG GAG	1178
Leu Leu Gly Gly Ile Gly Ile Ile His His Asn Cys Thr Ala Glu Glu	
90 95 100 105	
CAG GCG GAG ATG GTG CGC CGG GTC AAG AAG TAC GAA AAC GGG TTC ATC	1226
Gln Ala Glu Met Val Arg Arg Val Lys Lys Tyr Glu Asn Gly Phe Ile	
110 115 120	
AAC GCC CCC GTG GTC GTG GGG CCG GAC GCG ACG GTG GCG GAC GTG CGC	1274
Asn Ala Pro Val Val Val Gly Pro Asp Ala Thr Val Ala Asp Val Arg	
125 130 135	
CGG ATG AAG AAC GAG TTT GGG TTT GCA GGA TTT CCT GTG ACA	1316
Arg Met Lys Asn Glu Phe Gly Phe Ala Gly Phe Pro Val Thr	
140 145 150	
GGTATGTTAG AGTGGCACGC GGGGCTGCAC GCTGGGATGA TGATCATAAA TCAATAACTT	1376
TCGTTCTACT GACTGCGATC AAACGATCGT GTAGACACCT TTTACTCTGA CCGCAGACGT	1436

GCAGCGCCTT TTTGGCAGGA ACATGTACTA ACACATCAGC A GAT GAT GGC AAG	1489
Asp Asp Gly Lys	
1	
CCG ACC GGG AAG CTG CAG GGG ATC ATC ACG TCC CGT GAC ATC CAG TTT	1537
Pro Thr Gly Lys Leu Gln Gly Ile Ile Thr Ser Arg Asp Ile Gln Phe	
5 10 15 20	
GTC GAG GAC GAG ACC CTG CTT GTG TCT GAG ATC ATG ACC AAG GAC GTC	1585
Val Glu Asp Glu Thr Leu Leu Val Ser Glu Ile Met Thr Lys Asp Val	
25 30 35	
ATC ACT GGG AAG CAG GGC ATC AAC CTC GAG GAG GCG AAC CAG ATC CTG	1633
Ile Thr Gly Lys Gln Gly Ile Asn Leu Glu Glu Ala Asn Gln Ile Leu	
40 45 50	
AAG AAC ACC AAG AAG GGC AAG CTG CCA ATT GTG GAC GAG GCG GGC TGC	1681
Lys Asn Thr Lys Lys Gly Lys Leu Pro Ile Val Asp Glu Ala Gly Cys	
55 60 65	
CTG GTG TCC ATG CTT TCG AGA ACT GAC TTG ATG AAG AAC CAG TCC TAC	1729
Leu Val Ser Met Leu Ser Arg Thr Asp Leu Met Lys Asn Gln Ser Tyr	
70 75 80	
CCA TTG GCC TCC AAG TCT GCC GAC ACC AAG CAG CTG CTC TGT GGT GCT	1777
Pro Leu Ala Ser Lys Ser Ala Asp Thr Lys Gln Leu Leu Cys Gly Ala	
85 90 95 100	
GCG ATC GGC ACC ATC GAC GCG GAC AGG CAG AGA CTG GCG ATG CTG GTC	1825
Ala Ile Gly Thr Ile Asp Ala Asp Arg Gln Arg Leu Ala Met Leu Val	
105 110 115	
GAG GCC GGT CTG GAC GTT GTT GTG CTA GAC TCC TCG CAG GGT AAC TCG	1873
Glu Ala Gly Leu Asp Val Val Val Leu Asp Ser Ser Gln Gly Asn Ser	
120 125 130	
GTC TTC CAG ATC AAC ATG ATC AAG TGG ATC AAG GAG ACC TTC CCA GAC	1921
Val Phe Gln Ile Asn Met Ile Lys Trp Ile Lys Glu Thr Phe Pro Asp	
135 140 145	
CTG CAG GTC ATT GCT GGC AAC GTG GTC ACC AGA GAG CAG GCT GCC AGC	1969
Leu Gln Val Ile Ala Gly Asn Val Val Thr Arg Glu Gln Ala Ala Ser	
150 155 160	
TTG ATC CAC GCC GGC GCA GAC GGG TTG CGT ATC GGT ATG GGC TCT GGC	2017
Leu Ile His Ala Gly Ala Asp Gly Leu Arg Ile Gly Met Gly Ser Gly	
165 170 175 180	

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TCC ATC TGT ATC ACT CAG GAG GTG ATG GCC TGT GGT AGA CCA CAG GGT	2065
Ser Ile Cys Ile Thr Gln Glu Val Met Ala Cys Gly Arg Pro Gln Gly	
185 190 195	
ACC GCT GTC TAC AAC GTC ACG CAG TTC GCC AAC CAG TTT GGT GTG CCA	2113
Thr Ala Val Tyr Asn Val Thr Gln Phe Ala Asn Gln Phe Gly Val Pro	
200 205 210	
TGT ATT GCT GAC GGT GGT GTC CAG AAC ATC GGG CAC ATT ACC AAA GCT	2161
Cys Ile Ala Asp Gly Gly Val Gln Asn Ile Gly His Ile Thr Lys Ala	
215 220 225	
ATC GCT CTT GGC GCG TCC ACC GTC ATG ATG GGC GGT ATG CTG GCA GGC	2209
Ile Ala Leu Gly Ala Ser Thr Val Met Met Gly Gly Met Leu Ala Gly	
230 235 240	
ACT ACA GAG TCT CCA GGC GAG TAC TTC TTC AGG GAC GGG AAG AGA CTG	2257
Thr Thr Glu Ser Pro Gly Glu Tyr Phe Phe Arg Asp Gly Lys Arg Leu	
245 250 255 260	
AAG ACC TAC AGA GGT ATG GGC TCC ATC GAC GCC ATG CAA AAG ACT GAT	2305
Lys Thr Tyr Arg Gly Met Gly Ser Ile Asp Ala Met Gln Lys Thr Asp	
265 270 275	
GTC AAG GGT AAC GCC GCT ACC TCC CGT TAC TTC TCT GAG TCT GAC AAG	2353
Val Lys Gly Asn Ala Ala Thr Ser Arg Tyr Phe Ser Glu Ser Asp Lys	
280 285 290	
GTT CTG GTC GCT CAG GGT GTT ACT GGT TCT GTG ATC GAC AAG GGC TCC	2401
Val Leu Val Ala Gln Gly Val Thr Gly Ser Val Ile Asp Lys Gly Ser	
295 300 305	
ATC AAG AAG TAC ATT CCA TAT CTG TAC AAT GGT CTA CAG CAC TCG TGC	2449
Ile Lys Lys Tyr Ile Pro Tyr Leu Tyr Asn Gly Leu Gln His Ser Cys	
310 315 320	
CAG GAT ATC GGT GTG CGC TCT CTA GTG GAG TTC AGA GAG AAG GTG GAC	2497
Gln Asp Ile Gly Val Arg Ser Leu Val Glu Phe Arg Glu Lys Val Asp	
325 330 335 340	
TCT GGC TCG GTC AGA TTT GAG TTC AGA ACT CCA TCT GCC CAG TTG GAG	2545
Ser Gly Ser Val Arg Phe Glu Phe Arg Thr Pro Ser Ala Gln Leu Glu	
345 350 355	
GGT GGT GTG CAC AAC TTG CAC TCC TAC GAG AAG CGC CTA TTT GACTGAGTGC	2597
Gly Gly Val His Asn Leu His Ser Tyr Glu Lys Arg Leu Phe Asp	
360 365 370	
CACTAGGCCC AACTATAGA AGTGGATCCG GCGCGATGG CACCCATACT TTTATATTAT	2657

GTTGATTGAT GTACGTAAAC GATAGATATA ATAACAGACG CGGCATCTCA TTTGTATGCA 2717
 ATATATCTGG AACATGGTTA TGCCTACTCA ACTGTATGTA CTACTTTATA TACACAGCTC 2777
 TGGGACACTT GGTGAGATAT ATGTTTCATT ATGTATGCCT CGCTATCGAA AGGTCTGGCA 2837
 TTATGGGCTA CTGGGTCTAA GAGTCATGGC TTATGAGTAT TTATTTATTT ATTTCTCTTC 2897
 CTTTTCATTA AACTCCTCGA GCTTCTTTCT GTAATACTGC TCTCTAGACT TCTCCACATC 2957
 TGCTAATGAT GGTGGAAGTC GTTCGTTTTTC CAAATCCGCT CTACGAGCGC GCTCGAAGTT 3017
 AGACAGCGCC TCGTTCAGAC CTTCAGACCC GCGTGACAGC GCTCCACGAG GCAGCACGCC 3077
 AGAATTCATT GTTTTTAGGT ACTGCACCTT ATCGCTCTCT TCTCTCAACA CGCTATACAT 3137
 TCGGGAAACC TTGGCAATCG CCAATATTTT ACTGCGTAGT GCACGCCGTT TTGCATCATC 3197
 GTCCAGAATA GACCGTTTTT TCTTCGATTT CTTGGAGCCA GGTATAACAG TTACAACCTG 3257
 CTCAGTGTTT TTGGACTTCA ATGTAGCACC TAAGTCCTCC CTTATAACAA AAGTCTCTTC 3317
 CTCCAATTCT TCTTCAGTAC AAATGTTTAA TATCGAAACC AACATTTTCAG TCACTTTCTC 3377
 GCCAACAAAT GGCAAAGACC AGGTGAATAC GTCCATGAAA TTCGGTAACC AATACGGATG 3437
 CTGTGACATG TTAAATTGTC TAATGTTTAT AACGTTATCC GAGTATTTTA GGACCGCGGC 3497
 CTTGTTCTTG TAAGTGCCA AGTAGTTGGG TGCCTGAAC AACGTAAGTA AACTAGGAAA 3557
 GCCCAGATTC TTGGTATTCT TGTACATTCT GTAGCCCTGA TCTTGGGCTT CGTGGGCCC 3616

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met	Thr	Tyr	Arg	Asp	Ala	Ala	Thr	Ala	Leu	Glu	His	Leu	Ala	Thr	Tyr
1				5					10					15	
Ala	Glu	Lys	Asp	Gly	Leu	Ser	Val	Glu	Gln	Leu	Met	Asp	Ser	Lys	Thr
			20					25						30	

Arg Gly Gly Leu Thr Tyr Asn Asp Phe Leu Val Leu Pro Gly Lys Ile
 35 40 45
 Asp Phe Pro Ser Ser Glu Val Val Leu Ser Ser Arg Leu Thr Lys Lys
 50 55 60
 Ile Thr Leu Asn Ala Pro Phe Val Ser Ser Pro Met Asp Thr Val Thr
 65 70 75 80
 Glu Ala Asp Met Ala Ile His Met Ala Leu Leu Gly Gly Ile Gly Ile
 85 90 95
 Ile His His Asn Cys Thr Ala Glu Glu Gln Ala Glu Met Val Arg Arg
 100 105 110
 Val Lys Lys Tyr Glu Asn Gly Phe Ile Asn Ala Pro Val Val Val Gly
 115 120 125
 Pro Asp Ala Thr Val Ala Asp Val Arg Arg Met Lys Asn Glu Phe Gly
 130 135 140
 Phe Ala Gly Phe Pro Val Thr
 145 150

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Asp Asp Gly Lys Pro Thr Gly Lys Leu Gln Gly Ile Ile Thr Ser Arg
 1 5 10 15
 Asp Ile Gln Phe Val Glu Asp Glu Thr Leu Leu Val Ser Glu Ile Met
 20 25 30
 Thr Lys Asp Val Ile Thr Gly Lys Gln Gly Ile Asn Leu Glu Glu Ala
 35 40 45
 Asn Gln Ile Leu Lys Asn Thr Lys Lys Gly Lys Leu Pro Ile Val Asp
 50 55 60

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Glu Ala Gly Cys Leu Val Ser Met Leu Ser Arg Thr Asp Leu Met Lys
 65 70 75 80
 Asn Gln Ser Tyr Pro Leu Ala Ser Lys Ser Ala Asp Thr Lys Gln Leu
 85 90 95
 Leu Cys Gly Ala Ala Ile Gly Thr Ile Asp Ala Asp Arg Gln Arg Leu
 100 105 110
 Ala Met Leu Val Glu Ala Gly Leu Asp Val Val Val Leu Asp Ser Ser
 115 120 125
 Gln Gly Asn Ser Val Phe Gln Ile Asn Met Ile Lys Trp Ile Lys Glu
 130 135 140
 Thr Phe Pro Asp Leu Gln Val Ile Ala Gly Asn Val Val Thr Arg Glu
 145 150 155 160
 Gln Ala Ala Ser Leu Ile His Ala Gly Ala Asp Gly Leu Arg Ile Gly
 165 170 175
 Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Met Ala Cys Gly
 180 185 190
 Arg Pro Gln Gly Thr Ala Val Tyr Asn Val Thr Gln Phe Ala Asn Gln
 195 200 205
 Phe Gly Val Pro Cys Ile Ala Asp Gly Gly Val Gln Asn Ile Gly His
 210 215 220
 Ile Thr Lys Ala Ile Ala Leu Gly Ala Ser Thr Val Met Met Gly Gly
 225 230 235 240
 Met Leu Ala Gly Thr Thr Glu Ser Pro Gly Glu Tyr Phe Phe Arg Asp
 245 250 255
 Gly Lys Arg Leu Lys Thr Tyr Arg Gly Met Gly Ser Ile Asp Ala Met
 260 265 270
 Gln Lys Thr Asp Val Lys Gly Asn Ala Ala Thr Ser Arg Tyr Phe Ser
 275 280 285
 Glu Ser Asp Lys Val Leu Val Ala Gln Gly Val Thr Gly Ser Val Ile
 290 295 300
 Asp Lys Gly Ser Ile Lys Lys Tyr Ile Pro Tyr Leu Tyr Asn Gly Leu
 305 310 315 320
 Gln His Ser Cys Gln Asp Ile Gly Val Arg Ser Leu Val Glu Phe Arg
 325 330 335

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Glu Lys Val Asp Ser Gly Ser Val Arg Phe Glu Phe Arg Thr Pro Ser
 340 345 350

Ala Gln Leu Glu Gly Gly Val His Asn Leu His Ser Tyr Glu Lys Arg
 355 360 365

Leu Phe Asp
 370

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2697 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

- (ix) FEATURES:
 (A) NAME/KEY: 5'UTR
 (B) LOCATION: 1..455

- (ix) FEATURES:
 (A) NAME/KEY: CDS
 (B) LOCATION: 456..2033

- (ix) FEATURES:
 (A) NAME/KEY: 3'UTR
 (B) LOCATION: 2034..2697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

ATCGATTTC	GGAGATTTT	GGTAGCATT	TTGAGGTCAT	TAGAGGCGTT	CTGTGACTTT	60
CGACGATTG	CACGCGCAG	AGAGGGCGTT	CAACCAGCCT	TTCGGATATT	CCGGTTCGAG	120
TTATACCAG	CAGGATCAG	GCAGGCACT	GAGTGGCGGG	TGCTAATAAG	AGGAGCAGGT	180
CCTGGAACT	GAGTTGCAAG	AGATAAGCAT	TGCGCGGAGA	AGGAGGCGGT	TAGAGGGTGC	240
AAGCGAGCA	GATGGGGTCT	TCGATGAACT	TCCCGTCTGG	GTATGTGAAC	AAGCACACGC	300

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TGCAGGCACA	CCGGTAGGGC	GAGTGCAGGG	TGAAAAATAT	ATATGCGCTC	GAGAAGCGCT		360
GGGGATGAGT	TCGTCTGCAA	CGGCAGGCGG	ATCTTCATCT	GACAAAACCA	GCTGCCTACA		420
TCAGTGC	GAA GCTGTT	CAGT GATAGA	AATAG GAGTA	ATG GCT	GCT GTT	GAA CAA	473
				Met	Ala	Ala Val	
				1		5	
GTT TCT AGC GTG TTT GAC ACC ATT TTG GTG CTG GAC TTC GGG TCC CAG							521
Val Ser Ser Val Phe Asp Thr Ile Leu Val Leu Asp Phe Gly Ser Gln							
	10			15		20	
TAC TCG CAT CTG ATC ACG CGG CGG CTG CGT GAG TTT AAT GTG TAC GCG							569
Tyr Ser His Leu Ile Thr Arg Arg Leu Arg Glu Phe Asn Val Tyr Ala							
	25			30		35	
GAG ATG CTT CCG TGT ACG CAG AAG ATC AGC GAG CTG GGC TGG AAG CCA							617
Glu Met Leu Pro Cys Thr Gln Lys Ile Ser Glu Leu Gly Trp Lys Pro							
	40			45		50	
AAG GGT GTG ATT TTG TCA GGC GGG CCG TAC TCC GTG TAC GCG GCA GAT							665
Lys Gly Val Ile Leu Ser Gly Gly Pro Tyr Ser Val Tyr Ala Ala Asp							
	55			60		65	70
GCT CCG CAC GTG GAC CGG GCG GTG TTC GAG TTG GGC GTT CCA ATT CTG							713
Ala Pro His Val Asp Arg Ala Val Phe Glu Leu Gly Val Pro Ile Leu							
			75			80	85
GGC ATC TGC TAC GGG CTA CAG GAG CTT GCG TGG ATA GCC GGC GCA GAG							761
Gly Ile Cys Tyr Gly Leu Gln Glu Leu Ala Trp Ile Ala Gly Ala Glu							
			90			95	100
GTG GGG CGC GGC GAG AAG CGC GAG TAC GGG CGC GCG ACG CTG CAC GTG							809
Val Gly Arg Gly Glu Lys Arg Glu Tyr Gly Arg Ala Thr Leu His Val							
			105			110	115
GAG GAC AGC GCG TGC CCG CTG TTC AAC AAC GTG GAC AGC AGC ACG GTG							857
Glu Asp Ser Ala Cys Pro Leu Phe Asn Asn Val Asp Ser Ser Thr Val							
			120			125	130
TGG ATG TCG CAC GGT GAC AAG CTG CAC GCA CTA CCT GCG GAT TTC CAC							905
Trp Met Ser His Gly Asp Lys Leu His Ala Leu Pro Ala Asp Phe His							
			135			140	145
GTC ACT GCG ACG ACG GAG AAC TCT CCT TTC TGC GGG ATT GCA CAC GAC							953
Val Thr Ala Thr Thr Glu Asn Ser Pro Phe Cys Gly Ile Ala His Asp							
			155			160	165

TCG AAG CCA ATC TTC GGG ATC CAG TTC CAC CCT GAG GTG ACG CAC TCC	1001
Ser Lys Pro Ile Phe Gly Ile Gln Phe His Pro Glu Val Thr His Ser	
170 175 180	
TCG CAG GGG AAG ACG TTG CTG AAG AAC TTT GCG GTG GAG ATC TGC CAG	1049
Ser Gln Gly Lys Thr Leu Leu Lys Asn Phe Ala Val Glu Ile Cys Gln	
185 190 195	
GCC GCG CAG ACC TGG ACG ATG GAA AAC TTC ATT GAC ACC GAG ATC CAG	1097
Ala Ala Gln Thr Trp Thr Met Glu Asn Phe Ile Asp Thr Glu Ile Gln	
200 205 210	
CGG ATC CGG ACC CTT GTG GGC CCC ACC GCG GAA GTC ATC GGT GCT GTG	1145
Arg Ile Arg Thr Leu Val Gly Pro Thr Ala Glu Val Ile Gly Ala Val	
215 220 225 230	
TCC GGC GGT GTC GAC TCG ACC GTC GCT GCG AAG CTG ATG ACC GAG GCC	1193
Ser Gly Gly Val Asp Ser Thr Val Ala Ala Lys Leu Met Thr Glu Ala	
235 240 245	
ATC GGC GAC CGG TTC CAC GCG ATC CTG GTC GAC AAC GGT GTT CTG CGC	1241
Ile Gly Asp Arg Phe His Ala Ile Leu Val Asp Asn Gly Val Leu Arg	
250 255 260	
CTC AAC GAA GCG GCC AAT GTG AAG AAA ATC CTC GGC GAG GGC TTG GGC	1289
Leu Asn Glu Ala Ala Asn Val Lys Lys Ile Leu Gly Glu Gly Leu Gly	
265 270 275	
ATC AAC TTG ACT GTT GTT GAC GCC TCC GAA GAG TTC TTG ACG AAG CTC	1337
Ile Asn Leu Thr Val Val Asp Ala Ser Glu Glu Phe Leu Thr Lys Leu	
280 285 290	
AAG GGC GTC ACG GAC CCT GAG AAG AAG AGA AAG ATC ATC GGT AAC ACC	1385
Lys Gly Val Thr Asp Pro Glu Lys Lys Arg Lys Ile Ile Gly Asn Thr	
295 300 305 310	
TTC ATT CAT GTT TTT GAG CGC GAG GCA GCC AGG ATC CAG CCT AAG AAC	1433
Phe Ile His Val Phe Glu Arg Glu Ala Ala Arg Ile Gln Pro Lys Asn	
315 320 325	
GGC GAG GAG ATT GAG TTC CTG TTG CAG GGT ACC CTA TAC CCT GAC GTT	1481
Gly Glu Glu Ile Glu Phe Leu Leu Gln Gly Thr Leu Tyr Pro Asp Val	
330 335 340	
ATC GAG TCC ATT TCC TTT AAG GGC CCA TCT CAG ACG ATC AAG ACC CAC	1529
Ile Glu Ser Ile Ser Phe Lys Gly Pro Ser Gln Thr Ile Lys Thr His	
345 350 355	

CAT AAC GTC GGT GGT CTT TTG GAC AAC ATG AAA CTG AAG CTC ATT GAG	1577
His Asn Val Gly Gly Leu Leu Asp Asn Met Lys Leu Lys Leu Ile Glu	
360 365 370	
CCT TTG CGC GAG CTT TTC AAG GAC GAG GTG AGA CAC CTG GGA GAA CTA	1625
Pro Leu Arg Glu Leu Phe Lys Asp Glu Val Arg His Leu Gly Glu Leu	
375 380 385 390	
TTG GGG ATC TCC CAC GAG TTG GTC TGG AGA CAT CCG TTC CCA GGC CCA	1673
Leu Gly Ile Ser His Glu Leu Val Trp Arg His Pro Phe Pro Gly Pro	
395 400 405	
GGT ATC GCC ATC CGT GTG CTA GGC GAG GTC ACC AAG GAG CAG GTG GAG	1721
Gly Ile Ala Ile Arg Val Leu Gly Glu Val Thr Lys Glu Gln Val Glu	
410 415 420	
ATT GCC AGA AAG GCA GAC CAC ATC TAC ATC GAG GAG ATC AGG AAA GCA	1769
Ile Ala Arg Lys Ala Asp His Ile Tyr Ile Glu Glu Ile Arg Lys Ala	
425 430 435	
GGT CTA TAC AAC AAG ATT TCT CAA GCT TTT GCT TGC TTG CTG CCT GTT	1817
Gly Leu Tyr Asn Lys Ile Ser Gln Ala Phe Ala Cys Leu Leu Pro Val	
440 445 450	
AAG TCT GTG GGT GTC ATG GGT GAC CAG AGA ACC TAC GAC CAG GTC ATT	1865
Lys Ser Val Gly Val Met Gly Asp Gln Arg Thr Tyr Asp Gln Val Ile	
455 460 465 470	
GCT CTA AGA GCA ATT GAG ACC ACG GAC TTC ATG ACT GCC GAC TGG TAT	1913
Ala Leu Arg Ala Ile Glu Thr Thr Asp Phe Met Thr Ala Asp Trp Tyr	
475 480 485	
CCA TTT GAG CAC GAA TTC TTG AAG CAT GTC GCA TCC CGT ATT GTT AAC	1961
Pro Phe Glu His Glu Phe Leu Lys His Val Ala Ser Arg Ile Val Asn	
490 495 500	
GAG GTT GAA GGT GTT GCC AGA GTC ACC TAC GAC ATA ACT TCT AAG CCT	2009
Glu Val Glu Gly Val Ala Arg Val Thr Tyr Asp Ile Thr Ser Lys Pro	
505 510 515	
CCA GCT ACC GTT GAA TGG GAA TAATCACCCCT TGGGATCCGC TGA CTGGCTA	2060
Pro Ala Thr Val Glu Trp Glu	
520 525	
CTGTAATTCT ATGTAGTGA TTAGTACGAT AAGTTACTTT TGTATGATAG ATGTAATCAC	2120
ATCTGGCTAT TAAAATGACT CAGCCGAGGT AAATCTAACG TCCCTTCACA AGGGTGTTC	2180
TGTGTGGACT TCCGCCTGAA TTTTATAGA TATATAGATA CTCTACTCAT GAACAACCTG	2240

CAACCGAATA AGCATTAGTG CCAGGAGAAG AGAACCGTGG AAATGGGGCA AGTAGAAAAA 2300
 ATCATATTCC TTAAGAATAA GACAGTACCA GAGGACCATT ACGAGACGAT TTTTGAATCG 2360
 AATGGCTTCC AGACTCACTT TGTACCCATA ATAACCCATG AACACCTGCC AGATGAGGTT 2420
 CGCGGTCGAC TATCCGACGC GAATTACATG AAAAGGTTGA ATTGTTTGGT GGTAACCTCT 2480
 CAGAGGACTG TGGAGTGTCT CTATGAGGAC GTTCTGCCCT CTCTTCCAGC TGAAGCACGC 2540
 AAATCTCTTC TCAATACGCC AGTATTCGTG GTTGGGCGTG CCACTCAGGA ATTTATGGAG 2600
 AGATGCGGCT TTACGGACGT GAGAGGGGGA TCTGAGACTG GTAATGGCGT TTTGCTAGCG 2660
 GAGTTAATGT TAAATATGAT CCAGAAGGGC GATGGGG 2697

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Met Ala Ala Val Glu Gln Val Ser Ser Val Phe Asp Thr Ile Leu Val
 1 5 10 15
 Leu Asp Phe Gly Ser Gln Tyr Ser His Leu Ile Thr Arg Arg Leu Arg
 20 25 30
 Glu Phe Asn Val Tyr Ala Glu Met Leu Pro Cys Thr Gln Lys Ile Ser
 35 40 45
 Glu Leu Gly Trp Lys Pro Lys Gly Val Ile Leu Ser Gly Gly Pro Tyr
 50 55 60
 Ser Val Tyr Ala Ala Asp Ala Pro His Val Asp Arg Ala Val Phe Glu
 65 70 75 80
 Leu Gly Val Pro Ile Leu Gly Ile Cys Tyr Gly Leu Gln Glu Leu Ala
 85 90 95
 Trp Ile Ala Gly Ala Glu Val Gly Arg Gly Glu Lys Arg Glu Tyr Gly
 100 105 110

Arg Ala Thr Leu His Val Glu Asp Ser Ala Cys Pro Leu Phe Asn Asn
 115 120 125

Val Asp Ser Ser Thr Val Trp Met Ser His Gly Asp Lys Leu His Ala
 130 135 140

Leu Pro Ala Asp Phe His Val Thr Ala Thr Thr Glu Asn Ser Pro Phe
 145 150 155 160

Cys Gly Ile Ala His Asp Ser Lys Pro Ile Phe Gly Ile Gln Phe His
 165 170 175

Pro Glu Val Thr His Ser Ser Gln Gly Lys Thr Leu Leu Lys Asn Phe
 180 185 190

Ala Val Glu Ile Cys Gln Ala Ala Gln Thr Trp Thr Met Glu Asn Phe
 195 200 205

Ile Asp Thr Glu Ile Gln Arg Ile Arg Thr Leu Val Gly Pro Thr Ala
 210 215 220

Glu Val Ile Gly Ala Val Ser Gly Gly Val Asp Ser Thr Val Ala Ala
 225 230 235 240

Lys Leu Met Thr Glu Ala Ile Gly Asp Arg Phe His Ala Ile Leu Val
 245 250 255

Asp Asn Gly Val Leu Arg Leu Asn Glu Ala Ala Asn Val Lys Lys Ile
 260 265 270

Leu Gly Glu Gly Leu Gly Ile Asn Leu Thr Val Val Asp Ala Ser Glu
 275 280 285

Glu Phe Leu Thr Lys Leu Lys Gly Val Thr Asp Pro Glu Lys Lys Arg
 290 295 300

Lys Ile Ile Gly Asn Thr Phe Ile His Val Phe Glu Arg Glu Ala Ala
 305 310 315 320

Arg Ile Gln Pro Lys Asn Gly Glu Glu Ile Glu Phe Leu Leu Gln Gly
 325 330 335

Thr Leu Tyr Pro Asp Val Ile Glu Ser Ile Ser Phe Lys Gly Pro Ser
 340 345 350

Gln Thr Ile Lys Thr His His Asn Val Gly Gly Leu Leu Asp Asn Met
 355 360 365

Lys Leu Lys Leu Ile Glu Pro Leu Arg Glu Leu Phe Lys Asp Glu Val
 370 375 380

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Arg His Leu Gly Glu Leu Leu Gly Ile Ser His Glu Leu Val Trp Arg
 385 390 395 400
 His Pro Phe Pro Gly Pro Gly Ile Ala Ile Arg Val Leu Gly Glu Val
 405 410 415
 Thr Lys Glu Gln Val Glu Ile Ala Arg Lys Ala Asp His Ile Tyr Ile
 420 425 430
 Glu Glu Ile Arg Lys Ala Gly Leu Tyr Asn Lys Ile Ser Gln Ala Phe
 435 440 445
 Ala Cys Leu Leu Pro Val Lys Ser Val Gly Val Met Gly Asp Gln Arg
 450 455 460
 Thr Tyr Asp Gln Val Ile Ala Leu Arg Ala Ile Glu Thr Thr Asp Phe
 465 470 475 480
 Met Thr Ala Asp Trp Tyr Pro Phe Glu His Glu Phe Leu Lys His Val
 485 490 495
 Ala Ser Arg Ile Val Asn Glu Val Glu Gly Val Ala Arg Val Thr Tyr
 500 505 510
 Asp Ile Thr Ser Lys Pro Pro Ala Thr Val Glu Trp Glu
 515 520 525

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1634 Base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA for mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(ix) FEATURES:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..519

(ix) FEATURES:

- (A) NAME/KEY: CDS

(B) LOCATION: 520..1482

(ix) FEATURES:

(A) NAME/KEY: 3'UTR

(B) LOCATION: 1483..1634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCTCGAACAT CTATCTTCTG AGCTCGATAG TCTACGAAAT CGGCACACTA GCCTAATTGC	60
CGAGATGAAG AGCTCCAGGG AACCGTTAAA GATCTGATGT TCCATCTTCA ATCAGGACAA	120
ATGTTACGGG ATGTCCCTGA CGCCACAGAA GGTAGCCTGG TGGTCCAGAC AGAAAAAGAG	180
CCTACACCAA AGAAGAAACA TAACAAGAAA AAGCCTCCGC ATCGTTTTGG TAAATCATAA	240
TAGGCACGAT GCGCATATAC CCTGACCATC ATAGCGGTTC CCCCCGCTAA CTGCTCCGAG	300
CGGGTAACCC CATGTCACAA AGTGACTCTG TCTCTTCGTG GTAGGTGATG TCAAATTTTC	360
ACGACTTCCC ACCCCGATGA GCATCCGTAT TCCTTTTCAT CTAAATTCTA ATAGATGGCT	420
TATGGATTCT TATTGGCGAC TTACAAGCCT ATGTAGTTGG CTTCCCTCAA GTGTTCGTAG	480
TCTACCACCT CACACCCGGT CTAACAGCTT ACGAGAATA ATG GCT ACT AAT GCA	534
Met Ala Thr Asn Ala	
1 5	
ATC AAG CTT CTT GCG CCA GAT ATC CAC AGG GGT CTG GCA GAG CTG GTC	582
Ile Lys Leu Leu Ala Pro Asp Ile His Arg Gly Leu Ala Glu Leu Val	
10 15 20	
GCT AAA CGC CTA GGC TTA CGT CTG ACA GAC TGC AAG CTT AAG CGG GAT	630
Ala Lys Arg Leu Gly Leu Arg Leu Thr Asp Cys Lys Leu Lys Arg Asp	
25 30 35	
TGT AAC GGG GAG GCG ACA TTT TCG ATC GGA GAA TCT GTT CGA GAC CAG	678
Cys Asn Gly Glu Ala Thr Phe Ser Ile Gly Glu Ser Val Arg Asp Gln	
40 45 50	
GAT ATC TAC ATC ATC ACG CAG GTG GGG TCC GGG GAC GTG AAC GAC CGA	726
Asp Ile Tyr Ile Ile Thr Gln Val Gly Ser Gly Asp Val Asn Asp Arg	
55 60 65	
GTG CTG GAG CTG CTC ATC ATG ATC AAC GCT AGC AAG ACG GCG TCT GCG	774
Val Leu Glu Leu Leu Ile Met Ile Asn Ala Ser Lys Thr Ala Ser Ala	
70 75 80 85	
CGG CGA ATT ACG GCT GTG ATT CCA AAC TTC CCA TAC GCG CGG CAG GAC	822
Arg Arg Ile Thr Ala Val Ile Pro Asn Phe Pro Tyr Ala Arg Gln Asp	
90 95 100	

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CGG AAG GAT AAG TCA CGG GCG CCA ATT ACC GCG AAG CTC ATG GCG GAC	870
Arg Lys Asp Lys Ser Arg Ala Pro Ile Thr Ala Lys Leu Met Ala Asp	
105 110 115	
ATG CTG ACT ACC GCG GGC TGC GAT CAT GTC ATC ACC ATG GAC TTA CAC	918
Met Leu Thr Thr Ala Gly Cys Asp His Val Ile Thr Met Asp Leu His	
120 125 130	
GCT TCG CAA ATC CAG GGC TTC TTT GAT GTA CCA GTT GAC AAC CTT TAC	966
Ala Ser Gln Ile Gln Gly Phe Phe Asp Val Pro Val Asp Asn Leu Tyr	
135 140 145	
GCA GAG CCT AGC GTG GTG AAG TAT ATC AAG GAG CAT ATT CCC CAC GAC	1014
Ala Glu Pro Ser Val Val Lys Tyr Ile Lys Glu His Ile Pro His Asp	
150 155 160 165	
GAT GCC ATC ATC ATC TCG CCG GAT GCT GGT GGT GCC AAA CGT GCG TCG	1062
Asp Ala Ile Ile Ile Ser Pro Asp Ala Gly Gly Ala Lys Arg Ala Ser	
170 175 180	
CTT CTA TCA GAT CGC CTA AAC TTG AAC TTT GCG CTG ATT CAT AAG GAA	1110
Leu Leu Ser Asp Arg Leu Asn Leu Asn Phe Ala Leu Ile His Lys Glu	
185 190 195	
CGT GCA AAG GCA AAC GAA GTG TCC CGC ATG GTT CTG GTC GGC GAT GTT	1158
Arg Ala Lys Ala Asn Glu Val Ser Arg Met Val Leu Val Gly Asp Val	
200 205 210	
ACC GAT AAA GTC TGC ATT ATC GTT GAC GAT ATG GCG GAT ACT TGT GGT	1206
Thr Asp Lys Val Cys Ile Ile Val Asp Asp Met Ala Asp Thr Cys Gly	
215 220 225	
ACG CTG GCC AAG GCG GCA GAA GTG CTG CTA GAG CAC AAC GCG CGG TCT	1254
Thr Leu Ala Lys Ala Ala Glu Val Leu Leu Glu His Asn Ala Arg Ser	
230 235 240 245	
GTG ATA GCC ATT GTT ACC CAC GGT ATC CTT TCA GGA AAG GCC ATT GAG	1302
Val Ile Ala Ile Val Thr His Gly Ile Leu Ser Gly Lys Ala Ile Glu	
250 255 260	
AAC ATC AAC AAT TCG AAG CTT GAT AGG GTT GTG TGT ACC AAC ACC GTG	1350
Asn Ile Asn Asn Ser Lys Leu Asp Arg Val Val Cys Thr Asn Thr Val	
265 270 275	
CCA TTC GAG GAG AAG ATG AAG TTA TGC CCG AAG TTA GAT GTA ATT GAT	1398
Pro Phe Glu Glu Lys Met Lys Leu Cys Pro Lys Leu Asp Val Ile Asp	
280 285 290	
ATC TCG GCA GTT CTT GCG GAA TCC ATT CGC CGT CTA CAC AAT GGT GAA	1446
Ile Ser Ala Val Leu Ala Glu Ser Ile Arg Arg Leu His Asn Gly Glu	
295 300 305	

AGT ATC TCC TAC CTC TTT AAA AAC AAC CCA CTA TGATTTTGCT TCTCGATGCT 1499
 Ser Ile Ser Tyr Leu Phe Lys Asn Asn Pro Leu
 310 315 320

GGCTTCTTGA GGGCCAATTT TGCCGTAGAG GTAGTATCCC TTCTTTTTTAT ATTGACTATT 1559
 TAACGAAGAC TATTTCTTCA TAAATGGACT TCGGCTTCAC TGTGAATCTC ACATGATATA 1619
 GTTGTTTCAG AGACC 1634

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Met Ala Thr Asn Ala Ile Lys Leu Leu Ala Pro Asp Ile His Arg Gly
 1 5 10 15

Leu Ala Glu Leu Val Ala Lys Arg Leu Gly Leu Arg Leu Thr Asp Cys
 20 25 30

Lys Leu Lys Arg Asp Cys Asn Gly Glu Ala Thr Phe Ser Ile Gly Glu
 35 40 45

Ser Val Arg Asp Gln Asp Ile Tyr Ile Ile Thr Gln Val Gly Ser Gly
 50 55 60

Asp Val Asn Asp Arg Val Leu Glu Leu Leu Ile Met Ile Asn Ala Ser
 65 70 75 80

Lys Thr Ala Ser Ala Arg Arg Ile Thr Ala Val Ile Pro Asn Phe Pro
 85 90 95

Tyr Ala Arg Gln Asp Arg Lys Asp Lys Ser Arg Ala Pro Ile Thr Ala
 100 105 110

Lys Leu Met Ala Asp Met Leu Thr Thr Ala Gly Cys Asp His Val Ile
 115 120 125

Thr Met Asp Leu His Ala Ser Gln Ile Gln Gly Phe Phe Asp Val Pro
 130 135 140

Val Asp Asn Leu Tyr Ala Glu Pro Ser Val Val Lys Tyr Ile Lys Glu
 145 150 155 160

His Ile Pro His Asp Asp Ala Ile Ile Ile Ser Pro Asp Ala Gly Gly
 165 170 175

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Ala Lys Arg Ala Ser Leu Leu Ser Asp Arg Leu Asn Leu Asn Phe Ala		
180	185	190
Leu Ile His Lys Glu Arg Ala Lys Ala Asn Glu Val Ser Arg Met Val		
195	200	205
Leu Val Gly Asp Val Thr Asp Lys Val Cys Ile Ile Val Asp Asp Met		
210	215	220
Ala Asp Thr Cys Gly Thr Leu Ala Lys Ala Ala Glu Val Leu Leu Glu		
225	230	235 240
His Asn Ala Arg Ser Val Ile Ala Ile Val Thr His Gly Ile Leu Ser		
245	250	255
Gly Lys Ala Ile Glu Asn Ile Asn Asn Ser Lys Leu Asp Arg Val Val		
260	265	270
Cys Thr Asn Thr Val Pro Phe Glu Glu Lys Met Lys Leu Cys Pro Lys		
275	280	285
Leu Asp Val Ile Asp Ile Ser Ala Val Leu Ala Glu Ser Ile Arg Arg		
290	295	300
Leu His Asn Gly Glu Ser Ile Ser Tyr Leu Phe Lys Asn Asn Pro Leu		
305	310	315 320

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